Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1–9. (Canceled)

10. (Currently Amended) A method for determining a good or poor prognosis for a human patient suffering from neuroblastoma, the method comprising:

a. extracting biological material from a tumor or bone marrow sample taken from the patient;

b. contacting the biological material with reagents specific for a combination of 9 to 37 target genes comprising the nucleic acid sequences set forth in SEQ ID NOs: 1–37, wherein the reagents include at least reagents specific for the target genes comprising the nucleic acid sequences set forth in SEQ ID NOs: 2, 3, 7, 8, 10, 22, 25, 29, and 34, respectively;

c. determining expression levels of the target genes to obtain an expression profile for the patient; and

d. performing cluster analysis of the expression profile of the patient with expression profiles of the target genes from human patients previously clinically classified as good prognosis and expression profiles of the target genes from human patients previously clinically classified as poor prognosis, wherein:

a patient previously clinically classified as good prognosis is a patient diagnosed with a stage 1, 2, or 4s neuroblastoma and did not die within 75 months of diagnosis;

a patient previously clinically classified as poor prognosis is a patient diagnosed with a stage 4 neuroblastoma or died ~~within a~~ within 75 months of diagnosis;

if the expression profile of the patient is clustered with the expression profiles from patients previously clinically classified as good prognosis then the patient is determined to have a good prognosis; and

if the expression profile of the patient is clustered with the expression profiles from patients previously clinically classified as poor prognosis then the patient is determined to have a poor prognosis.

11. (Canceled)

12. (Previously Presented) The method according to claim 10, wherein the biological material extracted during step a) comprises nucleic acids.

13. (Previously Presented) The method according to claim 12, wherein at least one specific reagent of step b) comprises at least one hybridization probe.

14. (Previously Presented) The method according to claim 13, wherein at least one hybridization probe is immobilized on a support.

15. (Previously Presented) The method according to claim 14, wherein the support is a biochip.

16. (Withdrawn) The method according to claim 10, wherein, during step b), the biological material is brought into contact with reagents specific for a combination of 37 target genes comprising the nucleic acid sequences set forth in SEQ ID NOs:1 to 37, respectively.

17. (Withdrawn) The method according to claim 10, wherein, during step b), the biological material is brought into contact with reagents specific for a combination of 19 to 37 target genes comprising the nucleic acid sequences set forth in SEQ ID NOs:1–3, 7–10, 14, 16, 20–22, 25, 27, 29, 31, 34, 36, and 37, respectively.